Uncovering the Genetic Architecture of Spike Related Traits in Bread Wheat: A Viable Alternative to Increase Yield Potential

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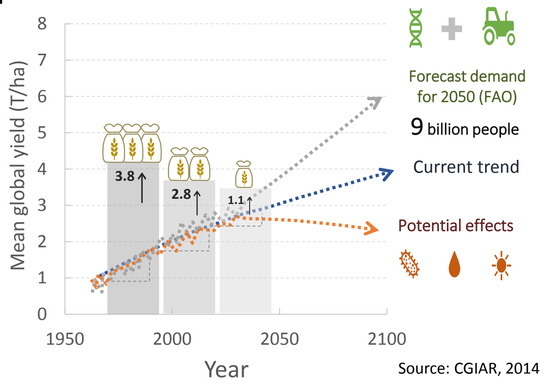
Introduction

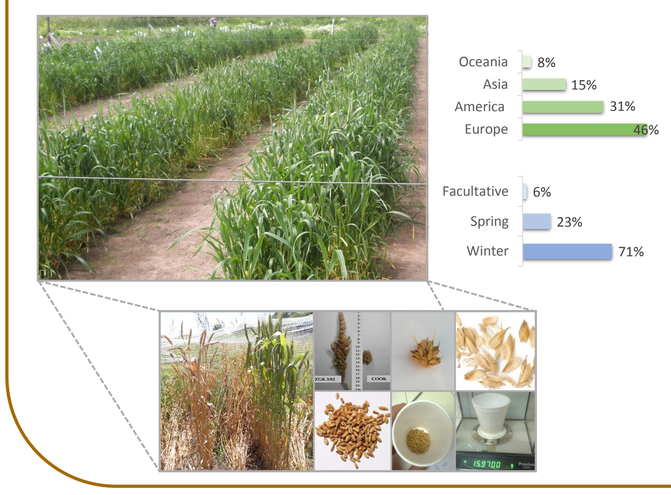
- Bread wheat supplies 20% of the world's daily protein and calories
- Further improvements in grain yield are required
- Production must increase by increasing grain yield potential
- Genetic diversity associated with yield related traits
- Yield is a complex trait
- The possible presence of trade-off between traits must be considered



Source: CGIAR, 2014

Material and methods

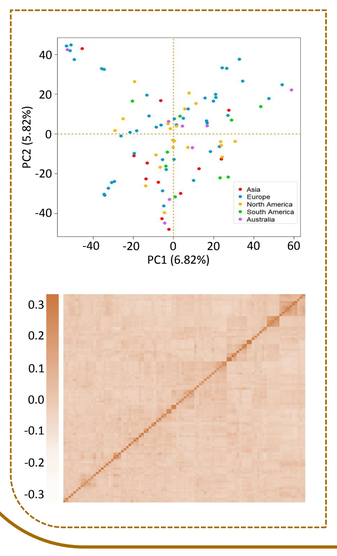
- Field experiments: (*i*) University of La Plata, La Plata, Argentina (LP) and (*ii*) Julio Hirschhorn Experimental Station, Los Hornos, Argentina (LH).



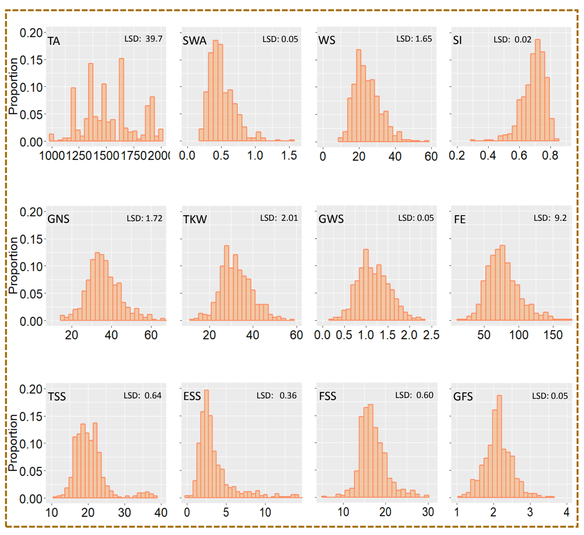
- Twelve spike related traits
- 15K Infinium SNP array
- The population structure
  Principal Components
- Phenotype–genotype association analysis
  -Mixed linear model (Tassel 5)
- IWGSC RefSeq v1.0

Results

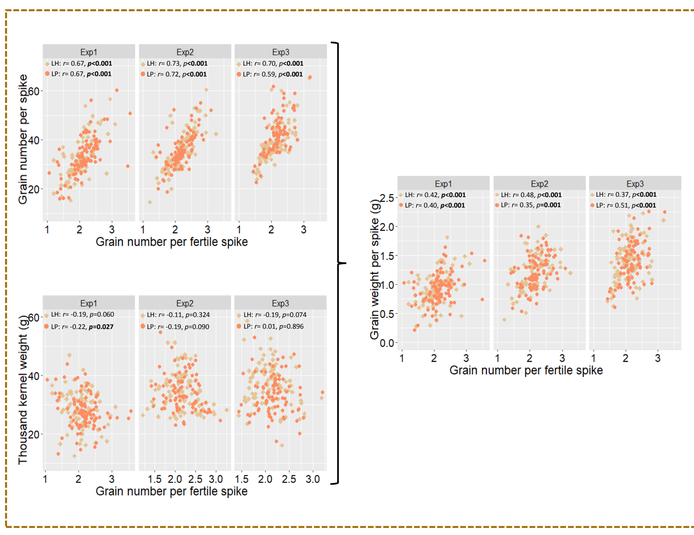
- Population structure and relationship matrix



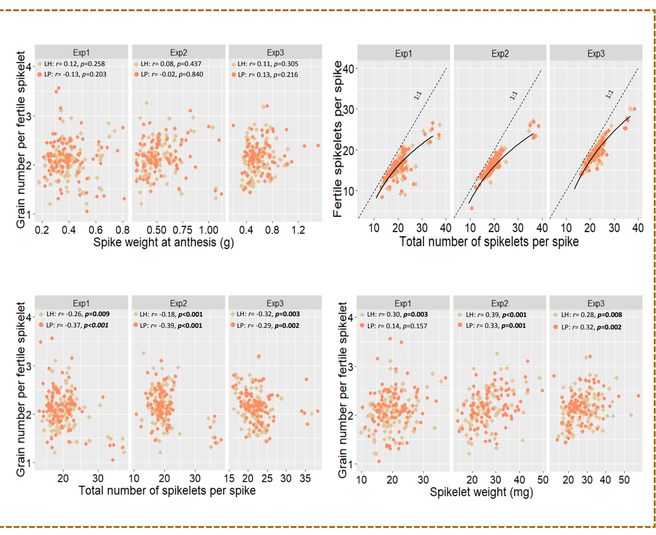
- The wheat population presented considerable phenotypic variation in all evaluated traits



- GFS showed the highest correlation with GNS, whereas there was no relationship with TKW. As a result, significant increases in GWS were observed



- GFS was mostly explained by SW, indicating that the partition within the spike can be improved

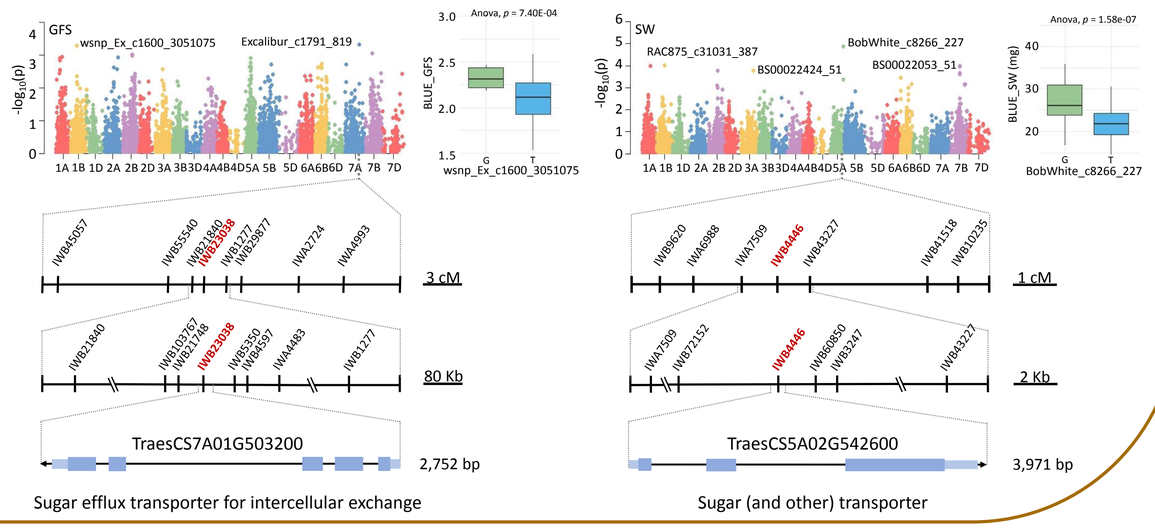


Results

- A total of 54 marker-trait associations were detected for spike related traits

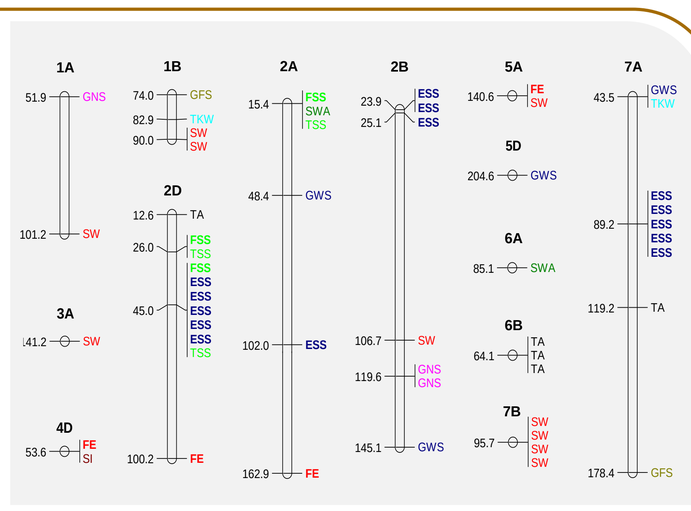
Trait	Marker	Chr	Pos	SNP	p-FDR	HC_Gene_IWGS_V1.1	Functional annotation
GNS	RAC875_c8245_272	1A	51.9	C/T	2.47E-04	TraesCS1A01G045300	Dual specificity phosphatase
SW	RAC875_c31031_387	1A	101.2	A/G	1.93E-04	TraesCS1A01G344400	Serine-threonine/tyrosine-protein kinase
GFS	wsnp_Ex_c1600_3051075	1B	74	T/G	5.20E-04	TraesCS1B01G303200	Protein of unknown function (DUF1668)
SW	BS00066944_51	1B	90	C/T	1.93E-04	Traes_1BL_C8ED70412	Leucine-rich repeat domain
TKW	BS00039740_51	1B	82.9	T/C	9.21E-05	TraesCS1B01G584200LC	.....
ESS	IACX6028	2A	102	C/T	5.40E-05	TraesCS2A01G138300	Cytochrome c oxidase subunit VII
FE	Tdurum_contig41912_893	2A	162.9	G/T	5.40E-05	.....	.....
GWS	BS00068050_51	2A	48.4	C/T	1.17E-04	TraesCS2A01G016200	.....
SWA	Jagger_c5341_126*	2A	15.4	A/G	1.49E-06	TraesCS2A02G040100	.....
ESS	BobWhite_c7145_355	2B	25.1	C/T	2.70E-04	TraesCS2B01G024600	.....
ESS	Kukri_c98858_299	2B	23.9	C/T	1.98E-04	TraesCS2B01G024600	.....
GNS	Tdurum_contig47_185	2B	119.6	C/T	1.59E-04	TraesCS2B01G541900	.....
GWS	Excalibur_rep_c83640_791	2B	145.1	T/C	3.45E-04	TraesCS2D01G053300	D-mannose binding lectin
SW	BS00100563_51	2B	106.7	A/G	2.48E-04	TraesCS2B01G397800	Small subunit of serine palmitoyltransferase
ESS	BS00080239_51	2D	45	C/T	2.90E-05	TraesCS2D01G139500	Heat shock protein DnaJ
FE	Kukri_rep_c68068_95	2D	100.2	G/A	7.56E-05	TraesCS2A01G567600	.....
FSS	CAP12_c1503_76*	2D	26	A/C	1.47E-05	TraesCS2D01G082700	Fatty acid desaturase
FSS	Excalibur_c5278_1075*	2D	45	T/G	1.47E-05	.....	.....
TA	JD_c63957_1176	2D	12.6	C/T	4.26E-04	Traes_2DS_70596CE28	.....
SW	BS00022424_51	3A	141.2	G/A	2.47E-04	TraesCS3A01G469400	Uncharacterized conserved protein (DUF2043)
FE	Kukri_rep_c68594_530*	4D	53.6	A/G	4.02E-04	TraesCS4D01G029200	Staphylococcal nuclease homologue
FE	BobWhite_c8266_227*	5A	140.6	T/G	8.78E-05	TraesCS5A01G542600	Sugar (and other) transporter
GWS	wsnp_Ex_c11055_17928283	5D	204.6	T/C	3.64E-04	TraesCS5D01G560900	.....
SWA	Tdurum_contig29629_437	6A	85.1	G/A	1.70E-04	TraesCS6A01G314100	FKBP-type peptidyl-prolyl cis-trans isomerase
TA	BS00063174_51	6B	64.1	G/T	2.57E-04	TraesCS6B01G190400	.....
ESS	Kukri_c106476_350	7A	89.2	C/T	1.89E-04	TraesCS7A01G101500	Inositol monophosphatase family
GFS	Excalibur_c1791_819	7A	178.4	C/T	4.89E-04	TraesCS7A01G503200	Sugar efflux transporter for intercellular exchange
GWS	tplb0032m13_1358	7A	43.5	C/T	3.64E-04	.....	.....
TA	RFL_Contig3425_378	7A	119.2	C/T	1.67E-04	TraesCS7A01G147300	Sugar efflux transporter for intercellular exchange
TKW	RAC875_c41169_68	7A	43.5	C/T	2.49E-04	TraesCS7A01G025800	ATPase family associated with cellular activities
SW	BS00022053_51	7B	95.7	A/C	1.93E-04	TraesCS7B01G375600	Peroxidase

- High Confidence genes based on the IWGSC RefSeq Annotation v1.0.



Results

- Independent genetic control between GFS and both, GNS and TKW
- Potential value of GFS as selection criterion to increase yield potential in wheat breeding programs



Conclusion

- Of the total of spike related traits, GFS showed the highest potential value to increase the grain yield potential in wheat breeding programs
- The markers linked to GFS and SW are really promising, especially considering that due to the destructive phenotypic determination, their improvement in early breeding generations can only be made by marker-assisted selection
- The reference wheat genome opened a new avenue to explore genome sequences, identify candidates genes and detect natural variations

Abbreviations

GFS: grain number per fertile spikelet
TSS: total number of spikelets per spike
FSS: number of fertile spikelets per spike
ESS: number of sterile spikelets per spike
TKW: thousand kernel weight
GNS: grain number per spike
GWS: grain weight per spike
SWA: spike weight at anthesis
FE: fruiting efficiency
TA: time to anthesis
SW: spikelet weight
SI: spike index